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OIPE

## RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/882,434A

TIME: 12:58:23

Input Set : A:\CULLN18seqtext.txt

Output Set: N:\CRF3\09182001\I882434A.raw

4 <110> APPLICANT: Manners, John M.  
 5 Marcus, John Paul  
 6 Goulter, Kenneth C.  
 7 Green, Jodie Lyn  
 9 <120> TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN  
 12 <130> FILE REFERENCE: CULLN18.1CP1C1  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/882,434A  
 C--> 14 <141> CURRENT FILING DATE: 2001-06-15  
 14 <150> PRIOR APPLICATION NUMBER: 09/364395  
 15 <151> PRIOR FILING DATE: 1999-07-30  
 17 <150> PRIOR APPLICATION NUMBER: 09/117615  
 18 <151> PRIOR FILING DATE: 1998-11-09  
 20 <150> PRIOR APPLICATION NUMBER: PCT/AU97/00052  
 21 <151> PRIOR FILING DATE: 1997-01-31  
 23 <150> PRIOR APPLICATION NUMBER: AU PN 7802  
 24 <151> PRIOR FILING DATE: 1996-01-31  
 26 <160> NUMBER OF SEQ ID NOS: 21  
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 102  
 32 <212> TYPE: PRT  
 33 <213> ORGANISM: Macadamia integrifolia  
 35 <400> SEQUENCE: 1  
 36 Met Ala Ser Thr Lys Leu Phe Phe Ser Val Ile Thr Val Met Met Leu  
 37 1 5 10 15  
 38 Ile Ala Met Ala Ser Glu Met Val Asn Gly Ser Ala Phe Thr Val Trp  
 39 20 25 30  
 40 Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu Arg Tyr Ser Lys Cys Gly  
 41 35 40 45  
 42 Cys Ser Ala Ile His Gln Lys Gly Gly Tyr Asp Phe Ser Tyr Thr Gly  
 43 50 55 60  
 44 Gln Thr Ala Ala Leu Tyr Asn Gln Ala Gly Cys Ser Gly Val Ala His  
 45 65 70 75 80  
 46 Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys Asn Pro Phe Gly Trp Lys  
 47 85 90 95  
 48 Ser Ile Phe Ile Gln Cys  
 49 100  
 51 <210> SEQ ID NO: 2  
 52 <211> LENGTH: 493  
 53 <212> TYPE: DNA  
 54 <213> ORGANISM: Macadamia integrifolia  
 56 <220> FEATURE:  
 57 <221> NAME/KEY: CDS  
 58 <222> LOCATION: (70)...(375)  
 59 <223> OTHER INFORMATION: y=t or c.  
 61 <400> SEQUENCE: 2  
 62 attaagtctt tgagtctcat acatactctt ctctctccca ccattagcac ttatcagcta 60

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63 acctcagcc atg gct tcc acc aag ttg ttc ttc tca gtc att act gtg atg      111
64      Met Ala Ser Thr Lys Leu Phe Phe Ser Val Ile Thr Val Met
65      1          5          10
67 atg ctc ata gca atg gca agt gag atg gtg aat ggg agt gca ttt aca      159
68 Met Leu Ile Ala Met Ala Ser Glu Met Val Asn Gly Ser Ala Phe Thr
69 15          20          25          30
71 gta tgg agt ggt cca ggt tgt aac aac cgt gct gag cga tat agc aag      207
72 Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu Arg Tyr Ser Lys
73          35          40          45
75 tgt gga tgc tca gct ata cat cag aag gga ggc tat gac ttc agc tac      255
76 Cys Gly Cys Ser Ala Ile His Gln Lys Gly Gly Tyr Asp Phe Ser Tyr
77          50          55          60
79 act gga caa act gct gct ctc tac aac cag gct gga tgc agt ggt gtt      303
80 Thr Gly Gln Thr Ala Ala Leu Tyr Asn Gln Ala Gly Cys Ser Gly Val
81          65          70          75
83 gca cac acc agg ttt ggg tcc agt gcc agg gca tgc aac cct ttt ggt      351
84 Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys Asn Pro Phe Gly
85          80          85          90
87 tgg aag agt atc ttc atc caa tgc tagatttcat aactcttgga tccatcttct      405
88 Trp Lys Ser Ile Phe Ile Gln Cys
89 95          100
91 atgttttttca agtgtataat tagagagatg catggatata taataaataa gtaaaagcta      465
92 cggtatcacc atgtgatgat tttyaccc      493
94 <210> SEQ ID NO: 3
95 <211> LENGTH: 19
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Degenerate primer alpha. ✓
102 <400> SEQUENCE: 3
103 ccgaagcagt tgcabgcgc      19
105 <210> SEQ ID NO: 4
106 <211> LENGTH: 20
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Degenerate primer beta. ✓
113 <400> SEQUENCE: 4
114 gagmgktatw skaagtgtgg      20
116 <210> SEQ ID NO: 5
117 <211> LENGTH: 20
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: 3' RACE primer alpha. ✓
124 <400> SEQUENCE: 5
125 tgctctctac aaccaggctg      20
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 19

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129 <212> TYPE: DNA  
 130 <213> ORGANISM: Artificial Sequence  
 132 <220> FEATURE:  
 133 <223> OTHER INFORMATION: 5' RACE primer beta. ✓  
 135 <400> SEQUENCE: 6  
 136 gcattggatg aagatactc 19  
 138 <210> SEQ ID NO: 7  
 139 <211> LENGTH: 36  
 140 <212> TYPE: DNA  
 141 <213> ORGANISM: Artificial Sequence  
 143 <220> FEATURE:  
 144 <223> OTHER INFORMATION: 5' RACE primer to anneal with poly-C-tailed cDNA ✓  
 145 primer alpha.  
 147 <221> NAME/KEY: misc\_feature  
 148 <222> LOCATION: (0)...(0)  
 149 <223> OTHER INFORMATION: n = inosine  
 151 <400> SEQUENCE: 7  
 W--> 152 ggccacgcgt cgactagtagtac gggnnngggnn gggngng ✓ 36  
 154 <210> SEQ ID NO: 8  
 155 <211> LENGTH: 20  
 156 <212> TYPE: DNA  
 157 <213> ORGANISM: Artificial Sequence  
 159 <220> FEATURE:  
 160 <223> OTHER INFORMATION: Mi28K primer. Mismatched oligonucleotide ✓  
 161 containing a mutation of the MiAMP1 coding  
 162 sequence from amino acid Q(position 28) to K.  
 164 <400> SEQUENCE: 8  
 165 gctatacata aaaagggagg 20  
 167 <210> SEQ ID NO: 9  
 168 <211> LENGTH: 20  
 169 <212> TYPE: DNA  
 170 <213> ORGANISM: Artificial Sequence  
 172 <220> FEATURE:  
 173 <223> OTHER INFORMATION: Mi39K primer. Mismatched oligonucleotide ✓  
 174 containing a mutation of the MiAMP1 coding  
 175 sequence from amino acid Q(position 39) to K.  
 177 <400> SEQUENCE: 9  
 178 tacactggaa aaactgctgc 20  
 180 <210> SEQ ID NO: 10  
 181 <211> LENGTH: 24  
 182 <212> TYPE: DNA  
 183 <213> ORGANISM: Artificial Sequence  
 185 <220> FEATURE:  
 186 <223> OTHER INFORMATION: Mi46K primer. Mismatched oligonucleotide ✓  
 187 containing a mutation of the MiAMP1 coding  
 188 sequence from amino acid Q(position 46) to K.  
 190 <400> SEQUENCE: 10  
 191 gcatccagct ttgttgtaga gagc 24  
 193 <210> SEQ ID NO: 11

## RAW SEQUENCE LISTING

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Input Set : A:\CULLN18seqtext.txt

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194 <211> LENGTH: 24
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Mi54V primer. Mismatched oligonucleotide ✓
200     containing a mutation of the MiAMP1 coding
201     sequence from amino acid H(position 54) to V.
203 <400> SEQUENCE: 11
204 ggtgttgtagcag tgaccaggtt tggg 24
206 <210> SEQ ID NO: 12
207 <211> LENGTH: 24
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Mi54K primer. Mismatched oligonucleotide ✓
213     containing a mutation of the MiAMP1 coding
214     sequence from amino acid H(position 54) to K.
216 <400> SEQUENCE: 12
217 ggtgttgcaa aaaccaggtt tggg 24
219 <210> SEQ ID NO: 13
220 <211> LENGTH: 31
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Oligonucleotide primer from the 5' coding region ✓
226     of MiAMP1 (Mi1 primer).
228 <400> SEQUENCE: 13
229 acaccatag agtgcattta cagtatgagt g 31
231 <210> SEQ ID NO: 14
232 <211> LENGTH: 35
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Oligonucleotide primer from the 3' coding region ✓
238     of MiAMP1 (Mi2 primer).
240 <400> SEQUENCE: 14
241 gaagagtatc ttcatccaat gctaaggatc cacac 35
243 <210> SEQ ID NO: 15
244 <211> LENGTH: 76
245 <212> TYPE: PRT
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Mi28K variant. Variant MiAMP1 protein Mi28K ✓
250     containing a Lysine at amino acid 28 (used primer
251     from SEQ ID NO:8 to produce).
253 <400> SEQUENCE: 15
254 Ser Ala Phe Thr Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu
255 1          5          10          15
256 Arg Tyr Ser Lys Cys Gly Cys Ser Ala Ile His Lys Lys Gly Gly Tyr

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257          20          25          30
258 Asp Phe Ser Tyr Thr Gly Gln Thr Ala Ala Leu Tyr Asn Gln Ala Gly
259          35          40          45
260 Cys Ser Gly Val Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys
261          50          55          60
262 Asn Pro Phe Gly Trp Lys Ser Ile Phe Ile Gln Cys
263 65          70          75
265 <210> SEQ ID NO: 16
266 <211> LENGTH: 76
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Mi39K variant. Variant MiAMP1 protein Mi39K ✓
272     containing a Lysine at amino acid 39 (used primer
273     from SEQ ID NO:9 to produce).
275 <400> SEQUENCE: 16
276 Ser Ala Phe Thr Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu
277 1          5          10          15
278 Arg Tyr Ser Lys Cys Gly Cys Ser Ala Ile His Gln Lys Gly Gly Tyr
279          20          25          30
280 Asp Phe Ser Tyr Thr Gly Lys Thr Ala Ala Leu Tyr Asn Gln Ala Gly
281          35          40          45
282 Cys Ser Gly Val Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys
283          50          55          60
284 Asn Pro Phe Gly Trp Lys Ser Ile Phe Ile Gln Cys
285 65          70          75
287 <210> SEQ ID NO: 17
288 <211> LENGTH: 76
289 <212> TYPE: PRT
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Mi46K variant. Variant MiAMP1 protein Mi46K ✓
294     containing a Lysine at amino acid 46 (used primer
295     from SEQ ID NO:10 to produce).
297 <400> SEQUENCE: 17
298 Ser Ala Phe Thr Val Trp Ser Gly Pro Gly Cys Asn Asn Arg Ala Glu
299 1          5          10          15
300 Arg Tyr Ser Lys Cys Gly Cys Ser Ala Ile His Gln Lys Gly Gly Tyr
301          20          25          30
302 Asp Phe Ser Tyr Thr Gly Gln Thr Ala Ala Leu Tyr Asn Lys Ala Gly
303          35          40          45
304 Cys Ser Gly Val Ala His Thr Arg Phe Gly Ser Ser Ala Arg Ala Cys
305          50          55          60
306 Asn Pro Phe Gly Trp Lys Ser Ile Phe Ile Gln Cys
307 65          70          75
309 <210> SEQ ID NO: 18
310 <211> LENGTH: 76
311 <212> TYPE: PRT
312 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/882,434A

DATE: 09/18/2001

TIME: 12:58:25

Input Set : A:\CULLN18seqtext.txt

Output Set: N:\CRF3\09182001\I882434A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7